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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      April 18, 2005, 09:14:43 ; Search time 73 Seconds
                                        (without alignments)
                                        5027.885 Million cell updates/sec

Title:           US-09-671-687A-3
Perfect score:   949
Sequence:        1 MSSGLWSQBKVTSPYWEERI.........RLLCDAYMCMYQSPTMSLYK 949
Scoring table:   OLIGO
                 Gapop 60.0 , Gapext 60.0
Searched:        2105692 seqs, 38676038l residues
Word size :      0

Total number of hits satisfying chosen parameters:     2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
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             2: geneseqp1990s:*
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             5: geneseqp2002s:*
             6: geneseqp2003as:*
             7: geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                  SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID		Description
1	606	63.9	685	4	AAM39254		Aam39254 Human pol
2	606	63.9	731	3	AAY91954		Aay91954 Human cyt
3	606	63.9	739	4	AAU23747		Aau23747 Novel hum
4	606	63.9	953	7	ADC24816		Adc24816 Human bre
5	606	63.9	953	8	ADQ95918		Adq95918 T cell ac
6	606	63.9	956	6	ABB82783		Abb82783 Human CYL
7	606	63.9	956	8	ADR14489		Adr14489 Human NF-
8	606	63.9	960	8	ADR99244		Adr99244 DKFZp586D
9	505	53.2	731	4	AAB95828		Aab95828 Human pro
10	505	53.2	953	8	ADQ95916		Adq95916 T cell ac
11	505	53.2	956	8	ADQ95920		Adq95920 T cell ac
12	363	38.3	698	4	AAM41040		Aam41040 Human pol
13	330	34.8	476	4	AAB95719		Aab95719 Human pro
14	227	23.9	558	4	AAU23211		Aau23211 Novel hum
15	208	21.9	261	5	ABB89233		Abb89233 Human pol
16	148	15.6	238	5	ABB89234		Abb89234 Human pol
17	113	11.9	113	4	AAM14965		Aam14965 Peptide #
18	113	11.9	113	4	ABB33941		Abb33941 Peptide #
19	113	11.9	113	4	AAM27399		Aam27399 Peptide #
20	113	11.9	113	4	ABB28754		Abb28754 Peptide #
21	113	11.9	113	4	ABB19377		Abb19377 Protein #
22	113	11.9	113	4	AAM67104		Aam67104 Human bon
23	113	11.9	113	4	AAM54704		Aam54704 Human bra
24	113	11.9	113	4	AAM02691		Aam02691 Peptide #
25	113	11.9	113	5	ABG36764		Abg36764 Human pep

26	106	11.2	106	8	ADK71947	Adk71947 Human ori
27	101	10.6	101	8	ADK71945	Adk71945 Human ori
28	96	10.1	96	8	ADK71949	Adk71949 Human ori
29	91	9.6	91	8	ADK71943	Adk71943 Human ori
30	91	9.6	104	8	ADK71962	Adk71962 Human ori
31	10	1.1	517	4	ABB61669	Abb61669 Drosophil
32	8	0.8	78	5	ABP68782	Abp68782 Marine sn
33	8	0.8	120	5	ADK35501	Adk35501 Novel hum
34	8	0.8	216	5	AAG72831	Aag72831 Human olf
35	8	0.8	228	7	ABO73471	Abo73471 Pseudomon
36	8	0.8	418	5	ABB64546	Abb64546 Drosophil
37	8	0.8	450	5	ABB50103	Abb50103 Listeria
38	8	0.8	450	6	ABU32881	Abu32881 Protein e
39	8	0.8	551	6	ABR83636	Abr83636 Saccharom
40	8	0.8	644	7	ADB80358	Adb80358 Human MDD
41	8	0.8	708	7	ABO71275	Abo71275 Pseudomon
42	8	0.8	941	7	ADF76391	Adf76391 Novel hum
43	8	0.8	1004	7	ADB80336	Adb80336 Human MDD
44	7	0.8	1086	8	ADN23310	Adn23310 Bacterial
45	7	0.7	18	5	AAO15840	Aao15840 CtxB sign

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                                          ALIGNMENTS

RESULT 1
AAM39254
ID   AAM39254 standard; protein; 685 AA.
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AC   AAM39254;
XX
DT   22-OCT-2001  (first entry)
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DE   Human polypeptide SEQ ID NO 2399.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;    99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSB-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,   Chen R,   Ma Y,   Qian XB,   Ren P,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,   Xue AJ,  Yang Y,   Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI58410.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 4; SEQ ID NO 2399; 10078pp; English.
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OM protein - protein search, using sw model

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                 GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: April 18, 2005, 09:18:24 ; Search time 57 Seconds
                                  (without alignments)
                            1242.841 Million cell updates/sec

Title: US-09-671-687A-3
Perfect score: 949
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Scoring table: OLIGO
                  Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size :   0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

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1	8	0.8	228	4	US-09-252-991A-22217	Sequence 22217, A
2	8	0.8	344	4	US-09-270-767-42367	Sequence 42367, A
3	8	0.8	708	4	US-09-252-991A-20021	Sequence 20021, A
4	8	0.8	2216	4	US-09-902-540-12221	Sequence 12221, A
5	7	0.7	28	3	US-09-227-357-607	Sequence 607, App
6	7	0.7	56	1	US-09-513-999C-6825	Sequence 6825, Ap
7	7	0.7	62	4	US-08-616-732A-24	Sequence 24, Appl
8	7	0.7	62	3	US-09-037-742B-24	Sequence 24, Appl
9	7	0.7	108	4	US-09-513-999C-6103	Sequence 6103, Ap
10	7	0.7	112	4	US-09-902-540-14754	Sequence 14754, A
11	7	0.7	116	2	US-08-879-995A-4	Sequence 4, Appli
12	7	0.7	116	3	US-09-215-096-4	Sequence 4, Appli
13	7	0.7	125	4	US-09-583-110-4643	Sequence 4643, Ap
14	7	0.7	127	4	US-09-513-999C-4224	Sequence 4224, Ap
15	7	0.7	134	4	US-09-107-433-2866	Sequence 2866, Ap
16	7	0.7	135	4	US-09-270-767-36133	Sequence 36133, A
17	7	0.7	135	4	US-09-270-767-51350	Sequence 51350, A
18	7	0.7	140	4	US-09-270-767-32498	Sequence 32498, A
19	7	0.7	140	4	US-09-270-767-47715	Sequence 47715, A
20	7	0.7	142	4	US-09-602-777A-334	Sequence 334, App
21	7	0.7	144	4	US-09-248-796A-18078	Sequence 18078, A
22	7	0.7	147	1	US-08-688-609-8	Sequence 8, Appli
23	7	0.7	147	3	US-09-002-832-8	Sequence 8, Appli
24	7	0.7	151	4	US-09-270-767-44667	Sequence 44667, A
25	7	0.7	151	4	US-09-902-540-15459	Sequence 15459, A
26	7	0.7	152	4	US-09-621-976-4852	Sequence 4852, Ap
27	7	0.7	153	4	US-09-270-767-56889	Sequence 56889, A
28	7	0.7	156	4	US-09-710-279-1222	Sequence 1222, Ap
29	7	0.7	162	4	US-09-270-767-33034	Sequence 33034, A
30	7	0.7	162	4	US-09-270-767-36622	Sequence 36622, A
31	7	0.7	162	4	US-09-270-767-48251	Sequence 48251, A
32	7	0.7	163	4	US-09-270-767-51839	Sequence 51839, A
33	7	0.7	163	2	US-08-783-395-5	Sequence 5, Appli
34	7	0.7	163	3	US-08-600-430-2	Sequence 2, Appli
35	7	0.7	163	3	US-09-134-001C-4131	Sequence 4131, Ap
36	7	0.7	163	4	US-09-461-912A-44	Sequence 44, Appl
37	7	0.7	163	4	US-09-949-016-6077	Sequence 6077, Ap
38	7	0.7	169	4	US-09-711-164-381	Sequence 381, App
39	7	0.7	172	4	US-09-270-767-41649	Sequence 41649, A
40	7	0.7	174	4	US-09-949-016-11208	Sequence 11208, A
41	7	0.7	181	4	US-09-513-999C-5797	Sequence 5797, Ap
42	7	0.7	185	4	US-09-583-110-4438	Sequence 4438, Ap
43	7	0.7	190	4	US-09-328-352-6627	Sequence 6627, Ap
44	7	0.7	192	4	US-09-107-433-3944	Sequence 3944, Ap
45	7	0.7	193	4	US-09-252-991A-17828	Sequence 17828, A

                              ALIGNMENTS

RESULT 1
US-09-252-991A-22217
; Sequence 22217, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22217
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22217

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  Best Local Similarity   100.0%; Pred. No. 27;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   164 VELLEEGR 171
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Db   151 VELLEEGR 158

RESULT 2
US-09-270-767-42367
; Sequence 42367, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42367
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-42367

  Query Match   0.8%; Score 8; DB 4; Length 344;
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OM protein - protein search, using sw model

Run on:       April 18, 2005, 09:40:40 ; Search time 57 Seconds
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Title:        US-09-671-687A-3
Perfect score: 949
Sequence:     1 MSSGLWSQEKVTSPYWEERI........RLLCDAYMCMYQSPTMSLYK 949

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched:     1421835 seqs, 332370683 residues

Word size :   0

Total number of hits satisfying chosen parameters:      1421835

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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          4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
          5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
          6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	606	63.9	731	16	US-10-921-707-9	Sequence 9, Appli
2	606	63.9	956	10	US-09-851-673-4	Sequence 4, Appli
3	606	63.9	956	16	US-10-755-889-490	Sequence 490, App
4	606	63.9	960	16	US-10-788-792-250	Sequence 250, App
5	208	21.9	261	15	US-10-264-237-1609	Sequence 1609, Ap
6	148	15.6	238	15	US-10-264-237-1610	Sequence 1610, Ap
7	113	11.9	113	9	US-09-864-761-34675	Sequence 34675, A
8	8	0.8	49	15	US-10-424-599-186263	Sequence 186263,
9	8	0.8	78	14	US-10-058-053A-218	Sequence 218, App
10	8	0.8	78	16	US-10-838-226-218	Sequence 218, App
11	8	0.8	122	16	US-10-437-963-180681	Sequence 180681,
12	8	0.8	143	15	US-10-424-599-170638	Sequence 170638,
13	8	0.8	188	15	US-10-424-599-159539	Sequence 159539,

14	8	0.8	371	16	US-10-437-963-188186	Sequence 188186,
15	8	0.8	450	15	US-10-282-122A-60805	Sequence 60805, A
16	8	0.8	1086	15	US-10-369-493-5963	Sequence 5963, Ap
17	7	0.7	28	10	US-09-983-802-607	Sequence 607, App
18	7	0.7	28	10	US-09-984-490-607	Sequence 607, App
19	7	0.7	28	11	US-09-973-278-461	Sequence 461, App
20	7	0.7	30	16	US-10-632-706-150	Sequence 150, App
21	7	0.7	30	16	US-10-632-706-154	Sequence 154, App
22	7	0.7	33	14	US-10-081-872-219	Sequence 219, App
23	7	0.7	33	15	US-10-385-305-219	Sequence 219, App
24	7	0.7	45	15	US-10-264-049-3820	Sequence 3820, Ap
25	7	0.7	53	15	US-10-613-413A-73	Sequence 73, Appl
26	7	0.7	53	17	US-10-885-225-73	Sequence 73, Appl
27	7	0.7	61	15	US-10-424-599-276896	Sequence 276896,
28	7	0.7	62	15	US-10-424-599-193894	Sequence 193894,
29	7	0.7	62	15	US-10-424-599-221399	Sequence 221399,
30	7	0.7	67	16	US-09-864-408A-6310	Sequence 6310, Ap
31	7	0.7	67	15	US-10-424-599-266715	Sequence 266715,
32	7	0.7	73	16	US-10-767-701-49557	Sequence 49557, A
33	7	0.7	79	16	US-10-437-963-184451	Sequence 184451,
34	7	0.7	82	16	US-10-767-701-61504	Sequence 61504, A
35	7	0.7	86	15	US-10-424-599-150683	Sequence 150683,
36	7	0.7	86	16	US-10-437-963-195228	Sequence 195228,
37	7	0.7	88	16	US-10-437-963-107983	Sequence 107983,
38	7	0.7	92	16	US-10-437-963-162456	Sequence 162456,
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42	7	0.7	104	16	US-10-767-701-48578	Sequence 48578, A
43	7	0.7	106	11	US-09-864-408A-2374	Sequence 2374, Ap
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ALIGNMENTS

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RESULT 1
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; Sequence 9, Application US/10921707
; Publication No. US2005003447A1
; GENERAL INFORMATION:
;   APPLICANT: INCYTE PHARMACEUTICALS, INC.
;   APPLICANT: LAL, Preeti
;   APPLICANT: TANG, Y. Tom
;   APPLICANT: YUE, Henry
;   APPLICANT: HILLMAN, Jennifer L.
;   APPLICANT: BANDMAN, Olga
;   APPLICANT: CORLEY, Neil C.
;   APPLICANT: GUEGLER, Karl J.
;   APPLICANT: PATTERSON, Chandra
;   APPLICANT: AZIMZAI, Yalda
;   APPLICANT: BAUGHN, Mariah R.
;   TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS
;   FILE REFERENCE: PF-0594 PCT
;   CURRENT APPLICATION NUMBER: US/10/921,707
;   CURRENT FILING DATE: 2004-08-19
;   PRIOR APPLICATION NUMBER: US/09/786,797
;   PRIOR FILING DATE: 2001-06-25
;   PRIOR APPLICATION NUMBER: 09/156,470; unassigned; 60/131,321
;   PRIOR FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: PERL Program
; SEQ ID NO 9
;   LENGTH: 731
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID NO: 2363327
US-10-921-707-9

Query Match          63.9%;  Score 606; DB 16; Length 731;
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                 GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:        April 17, 2005, 01:26:12 ; Search time 8968 Seconds
                                  (without alignments)
                               5127.565 Million cell updates/sec

Title:          US-09-671-687A-3
Perfect score:  949
Sequence:       1 MSSGLWSQEKVTSPYWEERI........RLLCDAYMCMYQSPTMSLYK 949

Scoring table:  OLIGO
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Searched:       4708233 seqs, 2422607955 residues

Word size:      1

Total number of hits satisfying chosen parameters:        9408497

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-UNITS=bits -START=-1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	754	79.5	3302	6	CQ834224	CQ834224 Sequence
2	754	79.5	3540	9	BC012342	BC012342 Homo sapi
3	754	79.5	5414	9	AB020656	AB020656 Homo sapi
4	711	74.9	4527	6	BD231207	BD231207 Human cyt

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6	667	70.3	3302	6	CQ834222	CQ834222 Sequence
7	641	67.5	2523	6	AR338799	AR338799 Sequence
8	640	67.4	3480	6	CQ719792	CQ719792 Sequence
9	608	64.1	2845	6	BD160617	BD160617 Primer fo
10	608	64.1	2845	6	AX883937	AX883937 Sequence
11	608	64.1	2845	6	AK024348	AK024348 Homo sapi
12	598	63.0	3311	9	CQ834226	CQ834226 Sequence
13	517	54.5	2341	9	AK000187	AK000187 Homo sapi
14	418	44.0	2569	6	BD160470	BD160470 Primer fo
15	418	44.0	2569	6	AX883681	AX883681 Sequence
16	418	44.0	2569	9	AK024212	AK024212 Homo sapi
17	374	39.4	1954	9	AK056226	AK056226 Homo sapi
18	165	17.4	2116	6	BD135433	BD135433 Receptor
19	165	17.4	2116	6	CQ867781	CQ867781 Sequence
20	165	17.4	2116	6	AR34837	AR34837 Sequence
21	165	17.4	2116	6	AX017216	AX017216 Sequence
22	140	14.8	141663	2	AC145018	AC145018 Felis cat
23	140	14.8	155857	2	AC145174	AC145174 Pan trogl
24	140	14.8	163319	9	AJ303140	AJ303140 Homo sapi
25 c	140	14.8	168271	9	AC007728	AC007728 Homo sapi
26	140	14.8	178790	2	AC145238	AC145238 Pan trogl
27	124	13.1	837	2	BD149741	BD149741 Primer fo
28	124	13.1	837	6	AX869679	AX869679 Sequence
29	123	13.0	758	2	BD147076	BD147076 Primer fo
30	123	13.0	758	6	AX867014	AX867014 Sequence
31	116	12.2	3267	10	BC082001	BC082001 Rattus no
32	116	12.2	4314	10	AK122389	AK122389 Mus muscu
33	116	12.2	4501	10	BC042438	BC042438 Mus muscu
34	109	11.5	241990	2	AC123449	AC123449 Rattus no
35 c	109	11.5	251132	2	AC098162	AC098162 Rattus no
36	108	11.4	251957	2	AC126867	AC126867 Rattus no
37	107	11.3	2426	10	BC049879	BC049879 Mus muscu
38 c	102	10.7	309	6	CQ055561	CQ055561 Sequence
39 c	102	10.7	309	6	CQ074825	CQ074825 Sequence
40 c	102	10.7	309	6	CQ105734	CQ105734 Sequence
41 c	102	10.7	309	6	CQ144418	CQ144418 Sequence
42 c	102	10.7	309	6	CQ179895	CQ179895 Sequence
43 c	102	10.7	309	6	CQ204266	CQ204266 Sequence
44 c	102	10.7	309	6	CQ265785	CQ265785 Sequence
45 c	102	10.7	309	6	CQ302867	CQ302867 Sequence

ALIGNMENTS

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DEFINITION  Sequence 95 from Patent WO2004058805.
ACCESSION   CQ834224
VERSION     CQ834224.1  GI:50833761
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Matsuda,A. and Yoneta,S.
  TITLE     T cell activating gene
  JOURNAL   Patent: WO 2004058805-A 95 15-JUL-2004;
            Asahi Kasei Pharma Corporation (JP)
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                          GenCore version 5.1.6
                  Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:      April 17, 2005, 01:25:02 ; Search time 1076. Seconds
                                       (without alignments)
                                       5221.036 Million cell updates/sec

Title:       US-09-671-687A-3
Perfect score: 949
Sequence:    1 MSSGLWSQBKVTSPYWEERI.........RLLCDAYMCMYQSPTMSLYK 949

Scoring table: OLIGO
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Searched:    4390206 seqs, 2959870667 residues

Word size:   1

Total number of hits satisfying chosen parameters:     8776198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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                            SUMMARIES
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	711	74.9	4527	3	AAA08589	Aaa08589 Human cyt
4	685	72.2	5371	10	ABV75394	Abv75394 Human CYL
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6	667	70.3	3302	12	ADQ95915	Adq95915 T cell ac
7	641	67.5	2523	4	AAI58410	Aai58410 Human pol
8	641	67.5	2523	5	ADQ98620	Adq98620 DNA encod
9	641	67.5	2523	9	ADB48380	Adb48380 Novel hum
10	641	67.5	4716	4	AAS41617	Aas41617 cDNA enco
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13	418	44.0	2569	4	AAH18478	Aah18478 Human CDN
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19	148	15.6	1013	6	ABL89643	Abl89643 Human pol
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21	123	13.0	758	4	AAH05084	Aah05084 Human CDN
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24c	102	10.7	309	4	AAI20692	Aai20692 Probe #10
25c	102	10.7	309	4	ABA65741	Aba65741 Human foe
26c	102	10.7	309	4	AAI45907	Aai45907 Probe #14
27c	102	10.7	309	4	ABA47848	Aba47848 Human bre
28c	102	10.7	309	4	ABA32825	Aba32825 Probe #11
29c	102	10.7	309	4	AAK39883	Aak39883 Human bon
30c	102	10.7	309	4	AAK14143	Aak14143 Human bra
31c	102	10.7	309	6	AAI06390	Aai06390 Probe #63
32c	102	10.7	309	5	ABS13981	Abs13981 Human gen
33	101	10.6	303	12	ADK71946	Adk71946 Human ori
34c	98	10.3	483	4	AAI11479	Aai11479 Probe #14
35c	98	10.3	483	4	ABA53149	Aba53149 Human foe
36c	98	10.3	483	4	AAI32754	Aai32754 Probe #14
37	98	10.3	483	4	ABA42721	Aba42721 Human bre
38	98	10.3	483	4	ABA22920	Aba22920 Probe #13
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                            ALIGNMENTS

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AC   ADQ95917;
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DT   07-OCT-2004  (first entry)
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DE   T cell activation associated cDNA #48.
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KW   ss; gene; antiallergic; antiarthritic; antiasthmatic; antidiabetic;
KW   anti-HIV; antimicrobial; antirheumatic; immunosuppressive;
KW   neuroprotective; gene therapy; T cell activation; diagnosis;
KW   autoimmune disease; rheumatoid arthritis; asthma; multiple sclerosis;
KW   diabetes; allergic disease; infectious disease; AIDS; chronic rejection;
KW   organ; bone-marrow transplant.
OS   Homo sapiens.
XX
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PD   15-JUL-2004.
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PF   25-DEC-2003; 2003WO-JP016715.
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                GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:       April 17, 2005, 06:40:33 ; Search time 377 Seconds
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Searched:        1202784 seqs, 818138359 residues

Word size:       1

Total number of hits satisfying chosen parameters:    2400006

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1		641	67.5	2523	4	US-09-620-312D-290	Sequence 290, App
2		165	17.4	2116	4	US-09-646-403-3	Sequence 3, Appli
3		36	3.8	110	4	US-09-513-999C-20085	Sequence 20085, A
4		9	0.9	747	3	US-08-998-416-246	Sequence 246, App
5		9	0.9	6574	3	US-09-221-017B-1097	Sequence 1097, Ap
6		9	0.9	20284	4	US-09-526-193A-21	Sequence 21, Appl
7		9	0.9	53806	4	US-09-949-016-12572	Sequence 12572, A
8	c	8	0.8	255	3	US-09-134-001C-2194	Sequence 2194, App
9	c	8	0.8	266	4	US-09-232-785-240	Sequence 240, App
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17	c	8	0.8	601	4	US-09-949-016-96111	Sequence 96111, A
18	c	8	0.8	601	4	US-09-949-016-192243	Sequence 192243,
19	c	8	0.8	601	4	US-09-949-016-195831	Sequence 195831,
20		8	0.8	687	4	US-09-252-991A-5646	Sequence 5646, Ap
21	c	8	0.8	702	4	US-09-252-991A-5549	Sequence 5549, Ap
22		8	0.8	771	4	US-09-902-540-3210	Sequence 3210, Ap
23		8	0.8	1030	4	US-09-621-976-18958	Sequence 18958, A
24		8	0.8	1098	4	US-09-270-767-10775	Sequence 10775, A
25	c	8	0.8	1164	4	US-09-107-532A-2278	Sequence 2278, Ap
26		8	0.8	1416	4	US-09-583-110-251	Sequence 251, App
27		8	0.8	1428	4	US-09-107-433-2425	Sequence 2425, Ap
28		8	0.8	1713	4	US-09-252-991A-3439	Sequence 3439, Ap
29	c	8	0.8	1938	4	US-09-252-991A-5524	Sequence 5524, Ap
30	c	8	0.8	2112	4	US-09-252-991A-3494	Sequence 3494, Ap
31	c	8	0.8	2127	4	US-09-252-991A-3450	Sequence 3450, Ap
32		8	0.8	2187	4	US-09-252-991A-5616	Sequence 5616, Ap
33		8	0.8	2481	4	US-09-902-540-5228	Sequence 5228, Ap
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35	c	8	0.8	3719	4	US-08-781-986A-344	Sequence 344, App
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37		8	0.8	5414	4	US-09-949-016-14322	Sequence 14322, A
38	c	8	0.8	5591	4	US-09-949-016-12044	Sequence 12044, A
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40		8	0.8	6651	4	US-09-358-383C-14	Sequence 14, Appl
41		8	0.8	7515	4	US-09-328-352-1695	Sequence 1695, Ap
42		8	0.8	7886	3	US-09-453-702B-102	Sequence 102, App
45		8	0.8	8729	3	US-09-453-702B-258	Sequence 258, App

ALIGNMENTS

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RESULT 1
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; Sequence 290, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Liu, Chenghua
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Zhang, Jie
;   APPLICANT: Ren, Feiyan
;   APPLICANT: Chen, Rui-hong
;   APPLICANT: Zhao, Qing A.
;   APPLICANT: Wehrman, Tom.
;   APPLICANT: Xue, Aidong J.
;   APPLICANT: Yang, Yonghong
;   APPLICANT: Wang, Jian-Rui
;   APPLICANT: Zhou, Ping
;   APPLICANT: Ma, Yunqing
;   APPLICANT: Wang, Dunrui
;   APPLICANT: Wang, Zhiwei
;   APPLICANT: John Tillinghast
;   APPLICANT: Drmanac, Radoje T.
;   TITLE OF INVENTION: No. 6569662el Nucleic Acids and
;   TITLE OF INVENTION: Polypeptides
;   FILE REFERENCE: 784CIP2B
;   CURRENT APPLICATION NUMBER: US/09/620,312D
;   CURRENT FILING DATE: 2000-07-19
;   PRIOR APPLICATION NUMBER: 09/552,317
;   PRIOR FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: 09/488,725
;   PRIOR FILING DATE: 2000-01-21
;   NUMBER OF SEQ ID NOS: 1105
;   SOFTWARE: pt_FL_genes Version 1.0
;   SEQ ID NO: 290
;     LENGTH: 2523
;     TYPE: DNA
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OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: April 17, 2005, 09:55:18 ; Search time 1145 Seconds
(without alignments)
5028.217 Million cell updates/sec

Title: US-09-671-687A-3
Perfect score: 949
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Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
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Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 3033355566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11234615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	711	74.9	4527	18	US-10-921-707-25	Sequence 25, Appl
	2	685	72.2	5371	10	US-09-851-673-3	Sequence 3, Appli
	3	685	72.2	5371	18	US-10-755-889-489	Sequence 489, App
	4	641	67.5	2523	15	US-10-037-270-290	Sequence 290, App
	5	641	67.5	2523	17	US-10-117-722-290	Sequence 290, App
	6	279	29.4	1151	17	US-10-264-237-204	Sequence 204, App
c	7	171	18.0	617	11	US-09-969-034-4253	Sequence 4253, Ap
c	8	165	17.4	2116	18	US-10-761-370-3	Sequence 3, Appli
	9	148	15.6	1013	17	US-10-264-237-205	Sequence 205, App
c	10	115	12.1	557	11	US-09-864-761-4254	Sequence 4254, Ap
c	11	102	10.7	309	9	US-09-864-761-18145	Sequence 18145, A
c	12	98	10.3	483	9	US-09-864-761-1386	Sequence 1386, Ap
	13	79	8.3	425	10	US-09-918-995-35878	Sequence 35878, A
	14	75	7.9	376	9	US-09-983-965-1633	Sequence 1633, Ap
	15	19	2.0	60	10	US-09-908-975-15332	Sequence 15332, A
	16	9	0.9	201	18	US-10-719-993-10379	Sequence 10379, A
	17	9	0.9	201	18	US-10-719-993-41266	Sequence 41266, A
	18	9	0.9	201	19	US-10-741-600-27452	Sequence 27452, A
	19	9	0.9	612	13	US-10-027-632-187795	Sequence 187795,
	20	9	0.9	612	17	US-10-027-632-187795	Sequence 187795,
c	21	9	0.9	661	9	US-09-919-580-881	Sequence 881, App
	22	9	0.9	842	18	US-10-425-115-90494	Sequence 90494, A
	23	9	0.9	1440	18	US-10-437-963-63191	Sequence 63191, A
	24	9	0.9	1863	17	US-10-424-599-31853	Sequence 31853, A
	25	9	0.9	4294	18	US-10-437-963-63187	Sequence 63187, A
	26	9	0.9	6574	13	US-10-194-163-1097	Sequence 1097, Ap
	27	9	0.9	9181	10	US-09-984-827-10	Sequence 10, Appl
	28	9	0.9	20284	17	US-10-452-510-21	Sequence 21, Appl
	29	9	0.9	20284	17	US-10-617-334-21	Sequence 21, Appl
	30	9	0.9	20284	18	US-10-744-465-21	Sequence 21, Appl
	31	9	0.9	20284	18	US-10-83-679-21	Sequence 21, Appl
c	32	9	0.9	83719	18	US-10-388-838-45	Sequence 45, Appl
	33	9	0.9	98146	18	US-10-322-281-126	Sequence 126, Appl
	34	9	0.9	159138	18	US-10-719-993-6777	Sequence 6777, Ap
	35	9	0.9	159138	19	US-10-741-600-17613	Sequence 17613, A
	36	9	0.9	174481	19	US-10-662-613-6	Sequence 6, Appli
	37	9	0.9	183999	18	US-10-745-377-1	Sequence 1, Appli
	38	9	0.9	183999	18	US-10-872-113-1	Sequence 1, Appli
	39	9	0.9	303172	18	US-10-719-993-6890	Sequence 6890, Ap
	40	8	0.8	25	19	US-10-719-900-49940	Sequence 49940, A
	41	8	0.8	25	19	US-10-719-900-271965	Sequence 271965,
	42	8	0.8	25	19	US-10-719-900-520291	Sequence 520291,
	43	8	0.8	25	19	US-10-719-900-555961	Sequence 555961,
c	44	8	0.8	25	19	US-10-719-900-737630	Sequence 737630,
c	45	8	0.8	148	17	US-10-424-599-43421	Sequence 43421, A

ALIGNMENTS

RESULT 1
US-10-921-707-25
; Sequence 25, Application US/10921707
; Publication No. US20050003447A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUSGLER, Karl J.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0594 PCT
; CURRENT APPLICATION NUMBER: US/10/921,707
; CURRENT FILING DATE: 2004-08-19

```
                   GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:     April 18, 2005, 09:17:58 ; Search time 22 Seconds
                                        (without alignments)
                                        4150.441 Million cell updates/sec

Title:          US-09-671-687A-3
Perfect score:  949
Sequence:       1 MSSGLWSQEKVTSPYWEERI.........RLLCDAYMCMYQSPTMSLYK 949
Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0

Searched:       283416 seqs, 96216763 residues

Word size :     0

Total number of hits satisfying chosen parameters:        283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :    PIR_79:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	1.3	727	2	S42834	F40F12.5 protein -
2	12	1.3	1021	2	F88568	protein F40F12.5 [
3	8	0.8	150	2	S65996	transcription regu
4	8	0.8	215	2	C83149	probable transcrip
5	8	0.8	448	2	T15188	hypothetical prote
6	8	0.8	450	2	AG1370	glucose-6-phosphat
7	8	0.8	450	2	AE1740	glucose-6-phosphat
8	8	0.8	458	2	D88950	protein R09B5.1 [i
9	8	0.8	486	2	C64765	yaiT protein precu
10	8	0.8	524	2	JS0746	cytochrome P450 1A
11	8	0.8	551	2	S63361	probable membrane
12	8	0.8	651	2	G83395	probable AMP-bindi
13	8	0.8	740	2	E69420	hydrogenase expres
14	8	0.8	760	2	F75530	ribonuclease - Dei
15	8	0.8	1086	2	T33893	hypothetical prote
16	8	0.7	50	2	A71570	hypothetical prote
17	7	0.7	72	2	G97134	hypothetical prote
18	7	0.7	81	2	C97140	hypothetical prote
19	7	0.7	104	2	T13628	tachykinin B precu
20	7	0.7	116	2	I65342	neurokinin B precu
21	7	0.7	116	2	A43779	probable tail comp
22	7	0.7	123	2	T09268	hypothetical prote
23	7	0.7	126	2	C82665	hypothetical prote
24	7	0.7	143	2	D71911	ribonuclease hi -
25	7	0.7	152	2	AI0448	probable ribonucle
26	7	0.7	152	2	A84303	hypothetical prote
27	7	0.7	157	2	S58012	probable olfactory
28	7	0.7	159	2	AD1590	hypothetical prote
29	7	0.7	163	2	JC5045	epithelial membran
30	7	0.7	169	2	C91130	hypothetical prote
31	7	0.7	169	2	C85975	hypothetical prote
32	7	0.7	169	2	A65103	pts system, n-acet
33	7	0.7	171	2	E95002	conserved hypothet
34	7	0.7	174	2	A45356	neuromedin U precu
35	7	0.7	177	2	F96739	hypothetical prote
36	7	0.7	178	2	A75578	hypothetical prote
37	7	0.7	179	2	AF1362	hypothetical prote
38	7	0.7	180	2	A69387	fumarase (fum-1) h
39	7	0.7	189	2	F90780	probable antirepre
40	7	0.7	189	2	B90820	antirepressor prot
41	7	0.7	189	2	A90852	antirepressor prot
42	7	0.7	189	2	B90874	probable antirepre
43	7	0.7	189	2	A90902	probable antirepre
44	7	0.7	189	2	B90911	probable antirepre
45	7	0.7	189	2	G90999	probable antirepre

ALIGNMENTS

```
RESULT 1
S42834
F40F12.5 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Nov-1999
C;Accession: S42834
R;Kershaw, J.
submitted to the EMBL Data Library, February 1994
A;Reference number: S42830
A;Accession: S42834
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-727 <KER>
A;Cross-references: EMBL:Z30215
C;Genetics:
A;Introns: 19/1; 53/2; 106/3; 156/2; 198/1; 358/2; 441/2; 678/3
C;Superfamily: Caenorhabditis elegans F40F12.5 protein

Query Match             1.3%;  Score 12;  DB 2;  Length 727;
Best Local Similarity  100.0%;  Pred. No. 0.0017;
Matches  12;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      856 AVLCIETSHYVA 867
            ||||||||||||
Db      592 AVLCIETSHYVA 603


RESULT 2
F88568
protein F40F12.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88568
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_e
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a:
A;Accession: F88568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1021 <STO>
A;Cross-references: GB:chr_III; PIDN:CAA82939.1; PID:g3877002; GSPDB:GN00021; CESP:F40
C;Genetics:
A;Gene: F40F12.5
A;Map position: 3

Query Match             1.3%;  Score 12;  DB 2;  Length 1021;
Best Local Similarity  100.0%;  Pred. No. 0.0023;
Matches  12;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

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OM protein - nucleic search, using frame_plus_p2n model

Run on:      April 17, 2005, 06:05:31 ; Search time 6188 Seconds
                                         (without alignments)
                             5837.588 Million cell updates/sec

Title:         US-09-671-687A-3
Perfect score: 949
Sequence:      1 MSSGLWSQEKVTSPYWEERI.........RLLCDAYMCMYQSPTMSLYK 949

Scoring table: OLIGO
               Xgapop 60.0 , Xgapext 60.0
               Ygapop 60.0 , Ygapext 60.0
               Fgapop  6.0 , Fgapext  .7.0
               Delop   6.0 , Delext   7.0

Searched:      34239544 seqs, 19032134700 residues

Word size:     1

Total number of hits satisfying chosen parameters:        68477535

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09671687/runat_15042005_163038_11962/app_query.fasta_1.1095
-DB=EST -QFMT=fastap -SUFFIX=Oligo.rst -MINMATCH=0_1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=Oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09671687_@CGN_1_5180_@runat_15042005_163038_11962 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=30 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_gss1:*
8: gb_gss1:*
9: gb_gss2:*

Result No.	Score	Query Match	Length	DB	ID	Description
1	387	40.8	3496	3	AF161542	Homo sapi
2	313	33.0	2862	9	AY406374	Homo sapi
3	312	32.9	2862	9	AY406375	Pan trogl
4	284	29.9	1039	4	BM457960	AGENCOURT
5	243	25.6	1063	5	BQ433523	AGENCOURT
6	237	25.0	726	7	CR772310	DKFZp468L
c 7	218	23.0	677	6	CD626856	56076837J
8	208	21.9	697	4	BM724143	UI-R-E01-
9	207	21.8	624	7	CN335014	170005319
10						CR789083 CR789083 7 601 21.1 200 CR789083 DKFZp468L
11						CB286853 CB286853 6 596 20.8 197 CB286853 CMD47_E07
12						BP226285 BP226285 5 575 19.9 189 BP226285 BP226285
c 13						CF528626 CF528626 7 581 19.9 189 CF528626 UI-1-BCl-
14						CD641429 CD641429 6 736 19.5 185 CD641429 AGENCOURT
15						BG180100 BG180100 5 919 18.9 179 BG180100 60232967S
16						BP219825 BP219825 5 583 18.8 178 BP219825 BP219825
17						CD639981 CD639981 6 689 18.4 175 CD639981 AGENCOURT
18						BM016881 BM016881 4 783 18.3 174 BM016881 60364338J
c 19						AA044899 AA044899 1 644 18.2 173 AA044899 zk75d10.s
20						BF724264 BF724264 2 510 17.9 170 BF724264 bx02g11.y
c 21						AA833748 AA833748 1 473 16.3 155 AA833748 od61b06.s
22						BP221754 BP221754 5 567 16.3 155 BP221754 BP221754
c 23						CD370161 CD370161 6 767 16.2 155 CD370161 UI-H-FT1-
24						BP221744 BP221744 5 573 16.2 154 BP221744 BP221744
25						BQ438227 BQ438227 5 907 16.1 153 BQ438227 AGENCOURT
c 26						AI130924 AI130924 1 425 14.9 141 AI130924 qc11a01.x
c 27						AA152263 AA152263 1 447 14.6 139 AA152263 z103a04.s
28						AA256728 AA256728 1 473 14.6 139 AA256728 zs22h05.r
29						CB466941 CB466941 4 708 14.4 137 CB466941 732655 MA
30						BI910868 BI910868 4 753 14.2 135 BI910868 60306751B
31						AA044687 AA044687 1 628 14.1 134 AA044687 zk75d10.r
32						BU570801 BU570801 5 1007 14.1 134 BU570801 AGENCOURT
c 33						AA761514 AA761514 1 406 14.0 133 AA761514 nz27d01.s
34						BG574981 BG574981 5 541 13.8 131 BG574981 602598070
c 35						AA056485 AA056485 4 569 13.8 131 AA056485 zk80b08.s
36						BM820463 BM820463 5 635 13.8 131 BM820463 K-EST0089
37						CD626855 CD626855 6 433 13.6 129 CD626855 56076837H
38						BM832976 BM832976 5 565 13.6 129 BM832976 K-EST0107
39						CB555752 CB555752 4 654 13.6 129 CB555752 MMSP0069
40						BM904688 BM904688 5 1134 13.6 129 BM904688 AGENCOURT
41						BI907475 BI907475 4 873 13.4 127 BI907475 60306357J
42						BG756164 BG756164 4 633 13.2 125 BG756164 60271346S
43						BP360904 BP360904 5 582 13.1 125 BP360904 BP360904
44						AU137267 AU137267 1 837 13.1 124 AU137267 AU137267
45						AU122742 AU122742 1 758 13.0 123 AU122742 AU122742

ALIGNMENTS

```
RESULT 1
AF161542
LOCUS       AF161542                3496 bp    mRNA    linear   HTC 22-MAY-2001
DEFINITION  Homo sapiens HSPC057 mRNA, complete cds.
ACCESSION   AF161542
VERSION     AF161542.1  GI:6841351
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3496)
  AUTHORS   Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G.,
            Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Gu,J., Chen,Z. and Chen,Z.
            Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.
  TITLE     Cloning and functional analysis of cDNAs with open reading frames
            for 300 previously undefined genes expressed in CD34+ hematopoietic
            stem/progenitor cells
  JOURNAL   Genome Res. 10 (10), 1546-1560 (2000)
  MEDLINE   20499367
   PUBMED   11042152
REFERENCE   2  (bases 1 to 3496)
  AUTHORS   Zhang,Q.H., Ye,M., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L.,
            Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.
  TITLE     Human full length cDNA cloned from cd34+ stem cells
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 3496)
  AUTHORS   Zhang,Q.H., Ye,M., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L.,
            Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-1999) Shanghai Institute of Hematology, Shanghai
            Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
            Shanghai 200025, P. R. China
```

us-09-671-687a-3.Oligo.rup

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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:        April 18, 2005, 09:15:43 ; Search time 65 Seconds
                                         (without alignments)
                                7476.356 Million cell updates/sec

Title:         US-09-671-687A-3
Perfect score: 949
Sequence:      1 MSSGLWSQEKVTSPYWEERI.........RLLCDAYMCMYQSPTMSLYK 949

Scoring table: OLIGO
               Gapop 60.0 , Gapext 60.0

Searched:      1612378 seqs, 512079187 residues

Word size :    0

Total number of hits satisfying chosen parameters:        1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :     UniProt_03:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                    SUMMARIES

Result        Query
No.    Score  Match Length DB ID           Description
-----  -----  ----- ------ -- ----         -----------
  1     606    606    956  1  CYLD_HUMAN   Q9nqc7 homo sapien
  2     116    116    952  1  CYLD_MOUSE   Q80tq2 mus musculu
  3     116    116    953  2  Q66H62       Q66h62 rattus norv
  4      98     98    454  2  Q6TXJ6       Q6txj6 rattus norv
  5      13     13    778  2  Q7Q4I4       Q7q4i4 anopheles g
  6      12     12    550  2  Q8IPC4       Q8ipc4 drosophila
  7      12     12    551  2  Q8IPC3       Q8ipc3 drosophila
  8      12     12    639  2  Q8IPC5       Q8ipc5 drosophila
  9      12     12    639  2  Q8SYF0       Q8syf0 drosophila
 10      12     12   1144  2  Q7JMS4       Q7jms4 caenorhabdi
 11      10     10    517  2  Q9VL04       Q9vl04 drosophila
 12       9      9    225  2  Q6AQ83       Q6aq83 desulfotale
 13       8      8     80  2  Q8EX39       Q8ex39 mycoplasma
 14       8      8    150  1  YYBA_BACSU   P37503 bacillus su
 15       8      8    212  2  Q7QYI6       Q7qyi6 giardia lam
 16       8      8    215  2  Q9HX43       Q9hx43 pseudomonas
 17       8      8    216  2  Q9GKF5       Q9gkf5 ornithorhyn
 18       8      8    225  2  Q7SFV2       Q7sfv2 neurospora
 19       8      8    236  2  Q9U0S3       Q9u0s3 nilaparvata
 20       8      8    237  2  Q8VXG1       Q8vxg1 lycopodiell
 21       8      8    258  2  Q7PJA3       Q7pja3 anopheles g
 22       8      8    274  2  Q62LG0       Q62lg0 burkholderi
 23       8      8    276  2  Q63WB0       Q63wb0 burkholderi
 24       8      8    353  2  Q9EZU8       Q9ezu8 serratia ma
 25       8      8    354  2  Q8N4A4       Q8n4a4 homo sapien
 26       8      8    366  2  Q6A178       Q6a178 cryptospori
 27       8      8    371  2  Q9AWT2       Q9awt2 oryza sativ
 28       8      8    401  2  Q6MJH4       Q6mjh4 bdellovibri
 29       8      8    418  2  Q9VHV0       Q9vhv0 drosophila
 30       8      8    423  2  O01754       O01754 caenorhabdi
 31       8      8    450  1  G6PI_LISIN   Q928r6 listeria in
 32       8      8    450  1  G6PI_LISMO   Q8y4r7 listeria mo
 33       8      8    450  2  Q71X61       Q71x61 listeria mo
 34       8      8    458  2  O44617       O44617    caenorhabdi
 35       8      8    522  2  Q6NAC1       Q6nac1 rhodopseudo
 36       8      8    524  1  CP11_MESAU   Q00557 mesocricetu
 37       8      8    551  1  AG12_YEAST   P53730 saccharomyc
 38       8      8    555  2  Q818V0       Q818v0 drosophila
 39       8      8    608  1  ACEK_RALSO   Q8y2q7 ralstonia s
 40       8      8    625  2  Q8K7W4       Q8k7w4 streptococc
 41       8      8    651  2  Q912B2       Q912b2 pseudomonas
 42       8      8    740  2  Q28905       Q28905 archaeoglob
 43       8      8    753  2  Q8F356       Q8f356 leptospira
 44       8      8    760  2  Q9RXG0       Q9rxg0 deinococcus
 45       8      8    763  2  Q72SG2       Q72sg2 leptospira
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                    ALIGNMENTS

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RESULT 1
CYLD_HUMAN
ID   CYLD_HUMAN     STANDARD;      PRT;   956 AA.
AC   Q9NQC7; O94934; Q7L3N6; Q96EH0; Q9NZX9;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable ubiquitin carboxyl-terminal hydrolase CYLD (EC 3.1.2.15)
DE   (Ubiquitin thiolesterase CYLD) (Ubiquitin-specific processing protease
DE   CYLD) (Deubiquitinating enzyme CYLD) (HSPC057).
GN   Name=CYLD; Synonyms=CYLD1, KIAA0849;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), DISEASE, AND TISSUE SPECIFICITY.
RX   MEDLINE=20296617; PubMed=10835629; DOI=10.1038/76006;
RA   Bignell G.R., Brown C., Biggs P.J., Lakhani S.R., Jones C., Hansen J.,
RA   Blair E., Hofmann B., Siebert R., Turner G., Evans D.G.,
RA   Schrander-Stumpel C., Beemer F.A., Van Den Ouweland A., Halley D.,
RA   Delpech B., Cleveland M.G., Leigh I., Leisti J., Rasmussen S.,
RA   Wallace M.R., Fenske C., Banerjee P., Oiso N., Chaggar R., Merrett S.,
RA   Leonard N., Huber M., Hohl D., Chapman P., Burn J., Swift S.,
RA   Smith A., Ashworth A., Stratton M.R.;
RT   "Identification of the familial cylindromatosis tumor suppressor
RT   gene.";
RL   Nat. Genet. 25:160-165(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RX   MEDLINE=99156230; PubMed=10048485;
RA   Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
RA   Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XII.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 5:355-364(1998).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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